

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 10:59:19 ; Search time 59.03 Seconds

(without alignments)
90.849 Million cell updates/sec

Title: US-09-785-059-2

Perfect score: 148
Sequence: 1 RVIRVORACRAIRHVRIRIGURLRVV 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeal:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 112 | 75.7 | 854 | 15 | 056319 simian-huma |
| 2 | 112 | 75.7 | 856 | 15 | 092877 simian-huma |
| 3 | 112 | 75.7 | 856 | 15 | 074599 human immun |
| 4 | 112 | 75.7 | 856 | 15 | 090587 human immun |
| 5 | 111 | 75.0 | 854 | 15 | 089797 human immun |
| 6 | 111 | 75.0 | 854 | 15 | 092762 human immun |
| 7 | 110 | 74.3 | 856 | 15 | 077694 human immun |
| 8 | 110 | 74.3 | 859 | 15 | 097694 human immun |
| 9 | 107 | 72.3 | 866 | 15 | 073301 human immun |
| 10 | 106 | 71.6 | 855 | 15 | 074841 human immun |
| 11 | 106 | 71.6 | 858 | 15 | 092874 human immun |
| 12 | 106 | 71.6 | 859 | 15 | 092937 human immun |
| 13 | 105 | 70.9 | 853 | 15 | 056108 human immun |
| 14 | 105 | 70.9 | 860 | 15 | 09DH01 human immun |
| 15 | 105 | 70.9 | 861 | 15 | 09E527 human immun |
| 16 | 105 | 70.9 | 861 | 15 | 09E523 human immun |

| | | | | | |
|----|-----|------|-----|----|--------------------|
| 17 | 105 | 70.9 | 862 | 15 | 093024 human immun |
| 18 | 104 | 70.3 | 860 | 15 | 09E534 human immun |
| 19 | 104 | 70.3 | 860 | 15 | 09E518 human immun |
| 20 | 104 | 70.3 | 872 | 15 | 091U21 human immun |
| 21 | 104 | 70.3 | 872 | 15 | 091U20 human immun |
| 22 | 103 | 69.6 | 357 | 15 | 078100 human immun |
| 23 | 103 | 69.6 | 853 | 15 | 056563 human immun |
| 24 | 103 | 69.6 | 856 | 15 | 074090 human immun |
| 25 | 103 | 69.6 | 862 | 15 | 09DVL5 human immun |
| 26 | 102 | 68.9 | 849 | 15 | 09PXE5 human immun |
| 27 | 102 | 68.9 | 853 | 15 | 073372 human immun |
| 28 | 102 | 68.9 | 858 | 15 | 071974 human immun |
| 29 | 102 | 68.9 | 858 | 15 | 091U25 human immun |
| 30 | 102 | 68.9 | 859 | 15 | 087924 human immun |
| 31 | 101 | 68.2 | 136 | 15 | 079566 human immun |
| 32 | 101 | 68.2 | 851 | 15 | 078243 human immun |
| 33 | 101 | 68.2 | 861 | 15 | 091U24 human immun |
| 34 | 101 | 68.2 | 869 | 15 | 073302 human immun |
| 35 | 101 | 68.2 | 869 | 15 | 090RE5 human immun |
| 36 | 101 | 68.2 | 883 | 15 | 090RE5 human immun |
| 37 | 100 | 67.6 | 856 | 15 | 0902G3 human immun |
| 38 | 100 | 67.6 | 860 | 15 | 073309 human immun |
| 39 | 100 | 67.6 | 863 | 15 | 041552 human immun |
| 40 | 99 | 66.9 | 56 | 15 | 056181 human immun |
| 41 | 99 | 66.9 | 56 | 15 | 056182 human immun |
| 42 | 99 | 66.9 | 56 | 15 | 056183 human immun |
| 43 | 99 | 66.9 | 56 | 15 | 056184 human immun |
| 44 | 99 | 66.9 | 56 | 15 | 056185 human immun |
| 45 | 99 | 66.9 | 56 | 15 | 056199 human immun |

ALIGNMENTS

RESULT 1
ID 056319 PRELIMINARY: PRT: 854 AA.
AC 056319;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ENV.
GN ENV.
OS Simian-Human Immunodeficiency virus.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=57667;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SHIV-89.6;
RA Reimann K.A., Li J.T., Voss G., Lekutis C., Tenner-Racz K., Racz P., Lin W., Montefiori D.C., Lee-Parritz D.E., Lu Y., Collman R.G., Sodroski J., Letvin N.L.;
RT An env gene derived from a primary human immunodeficiency virus type 1 isolate confers high in vivo replicative capacity to a chimeric simian/human immunodeficiency virus in rhesus monkeys.;
RL J. Virol. 70:3198-3206(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-SHIV-89.6;
RA Reimann K.A., Li J.T., Voss G., Lekutis C., Tenner-Racz K., Racz P., Lin W., Montefiori D.C., Lee-Parritz D.E., Lu Y., Collman R.G., Sodroski J., Letvin N.L.;
RT Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF038398; AAB9966.1; -
DR InterPro: IPR00328; Env_GPA1.
DR InterPro: IPR00777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GPA1; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 854 AA; 97265 MW; 72AAB153IDICFA7 CRC64;


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AC 073301;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE ENVELOPE GLYCOPROTEIN.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96263682; PubMed=8924250;
RA Douglas N.W., Knight A.I., Hayhurst A., Barrett W.Y., Kevany M.J.,
RA Daniels R.S.;
RT "An efficient method for the rescue and analysis of functional HIV-1
RT env genes: evidence for recombination in the vicinity of the tat/rev
RT splice site.";
RL AIDS 10:39-46(1996).
DR EMBL; U36875; AAC5535.1; -.
DR InterPro; IPR000328; Env_Gp41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 866 AA; 98348 MW; 6482AF2FED4BD4A0 CRC64;

Query Match 72.3%; Score 107; DB 15; Length 866;
Best Local Similarity 75.9%; Pred. No. 1.8e-06;
Matches 22; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RVIRVORACRAIRHIVRIRIROGLRRL 29
Db 838 RVIEVGRACRAIRHIVRIRIROGLRRLQ 866

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RESULT 10
Q74841
ID 074841 PRELIMINARY; PRT; 855 AA.
AC 074841;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE ENV.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90303973; PubMed=2364020;
RA Suenemann U., Schneider J., Mous J., Brunckhorst U., Schedel I.,
RA Jentsch K.D., Hunsmann G.;
RT "Molecular cloning and characterization of a German HIV-1 isolate.";
RL AIDS Res. Hum. Retroviruses 6:813-823(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HAN-2;
RA Bryant B.W.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U43141; AAA85237.1; -.
DR InterPro; IPR000328; Env_Gp41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 855 AA; 97507 MW; EF3CB615A23992F9 CRC64;

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Query Match 71.6%; Score 106; DB 15; Length 855;
 Best Local Similarity 78.6%; Pred. No. 2.5e-06;
 Matches 22; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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Qy 1 RVIRVORACRAIRHIVRIRIROGLRRL 28
Db 827 RVIEVGRACRAIRHIVRIRIROGLRRL 854

RESULT 11
Q92874
ID 092874 PRELIMINARY; PRT; 858 AA.
AC 092874;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE ENVELOPE GLYCOPROTEIN.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=PHI146;
RL MEDLINE=99372987; PubMed=10445815;
RA Ataman-Onal Y., Collier C., Giraud A., Babic-Erceg A., Biton F.,
RA Verrier B.;
RT "Comparison of complete env gene sequences from individuals with
RT symptomatic primary HIV type 1 infection.";
RL AIDS Res. Hum. Retroviruses 15:1035-1039(1999).
DR EMBL; AF041127; AAC02518.1; -.
DR InterPro; IPR000328; Env_Gp41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 858 AA; 97396 MW; 8E43A641C9D1535F CRC64;

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Query Match 71.6%; Score 106; DB 15; Length 856;
Best Local Similarity 78.6%; Pred. No. 2.5e-06;
Matches 22; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RVIRVORACRAIRHIVRIRIROGLRRL 28
Db 830 RVIEVGRACRAIRHIVRIRIROGLRRL 857

RESULT 12
Q92937
ID 092937 PRELIMINARY; PRT; 859 AA.
AC 092937;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE ENVELOPE GLYCOPROTEIN.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HIV-1JC;
RX MEDLINE=98440562; PubMed=9765443;
RA Mwaengo D.M., Novembre F.J.;
RT "Molecular cloning and characterization of viruses isolated from
RT chimpanzees with pathogenic human immunodeficiency virus type 1
RT infections.";
RL J. Virol. 72:8976-8987(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HIV-1JC;
RA Mwaengo D.M., Novembre F.J.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF049494; AAC68848.1; -.
DR InterPro; IPR000328; Env_Gp41.

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DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 859 AA; 97811 MW; E43A24C8424B6B2 CRC64;

Query Match
Best Local Similarity 71.6%; Score 106; DB 15; Length 859;
Matches 22; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 RVIRVORACRAIRHIVRIRROGLRRIL 28
DB 831 RIVELVGRACRAIRHIVRIRROGLRRIL 858

RESULT 13
ID 056108 PRELIMINARY; PRT; 853 AA.
AC 056108;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ENVELOPE GLYCOPROTEIN.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-SEMS3.1;
RX MEDLINE=98178716; PubMed=9519894;
RA McCutchan F.E., Sanders-Buell E., Salminen M.O., Carr J.K.,
RA Sheppard W.H.;
RT "Diversity of the human immunodeficiency virus type 1 envelope
RT glycoprotein in San Francisco Men's Health Study participants.";
RL AIDS Res. Hum. Retroviruses 14:329-337(1998).
DR EMBL: AF025751; AAC40589.1; -.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 853 AA; 96830 MW; EC8BA4418F8AEC47 CRC64;

Query Match
Best Local Similarity 70.9%; Score 105; DB 15; Length 853;
Matches 22; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 RVIRVORACRAIRHIVRIRROGLRRIL 28
DB 825 RIVELVGRACRAIRHIVRIRROGLRRIL 852

RESULT 14
ID 09DH01 PRELIMINARY; PRT; 860 AA.
AC 09DH01;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE ENV PROTEIN.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20457217; PubMed=11000225;
RA Yuste E., Lopez-Galindez C., Domingo E.;
RT "Unusual Distribution of Mutations Associated with Serial Bottleneck
RT Passages of Human Immunodeficiency Virus Type 1.";

RL J. Virol. 74:9546-9552(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Yuste E., Lopez-Galindez C., Domingo E.;
RL Submitted (Apr-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF256211; AAG16849.1; -.
DR EMBL: AF256205; AAG16800.1; -.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 860 AA; 97682 MW; 9635DF9832F8A32 CRC64;

Query Match
Best Local Similarity 70.9%; Score 105; DB 15; Length 860;
Matches 22; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 RVIRVORACRAIRHIVRIRROGLRRIL 29
DB 832 RIVELVGRACRAIRHIVRIRROGLRRIL 860

RESULT 15
ID 09E527 PRELIMINARY; PRT; 861 AA.
AC 09E527;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ENV PROTEIN.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20457217; PubMed=11000225;
RA Yuste E., Lopez-Galindez C., Domingo E.;
RT "Unusual Distribution of Mutations Associated with Serial Bottleneck
RT Passages of Human Immunodeficiency Virus Type 1.";
RL J. Virol. 74:9546-9552(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Yuste E., Lopez-Galindez C., Domingo E.;
RL Submitted (Apr-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF256206; AAG16808.1; -.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
SQ SEQUENCE 861 AA; 97645 MW; DD0D135B595424E8 CRC64;

Query Match
Best Local Similarity 70.9%; Score 105; DB 15; Length 861;
Matches 22; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 RVIRVORACRAIRHIVRIRROGLRRIL 29
DB 833 RIVELVGRACRAIRHIVRIRROGLRRIL 861

Search completed: August 14, 2002, 10:59:20
Job time: 516 sec

